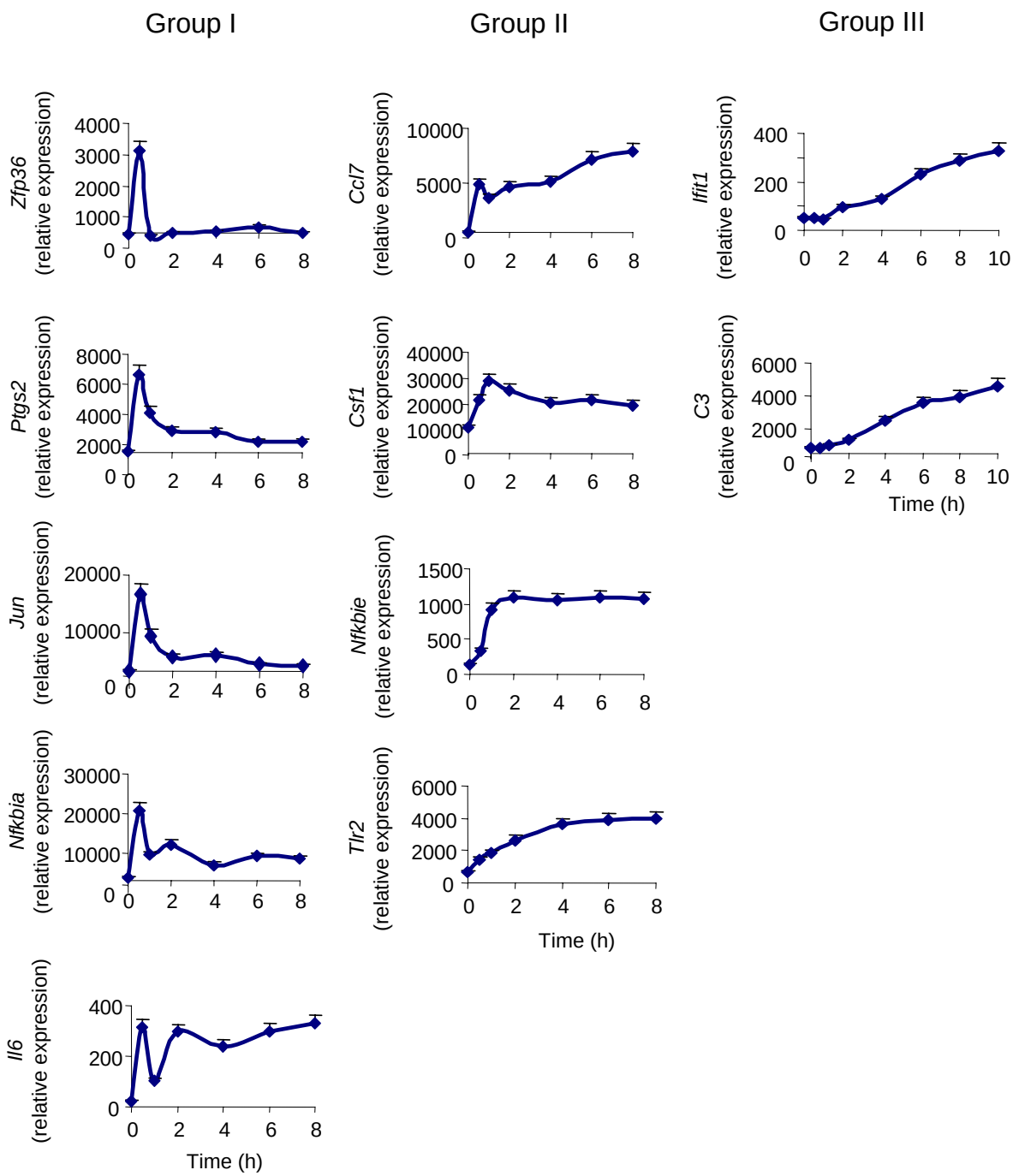
Supplementary Figure 1. Additional examples of genes within the three groups of TNF-activated genes. 3T3 fibroblasts were stimulated with TNF (10 ng/ml). At indicated times after addition of TNF, mRNA transcripts encoding genes in each group were measured by RT-qPCR and normalized to *Rpl32* as described in **Methods**. The results are shown as mean ± s.d. of triplicate samples and representative of four independent experiments with similar results.

Supplementary Figure 2. Kinetic patterns of TNF-induced gene expression in human dermal primary fibroblasts. Cells were exposed to continual TNF (10 ng/ml) stimulation (TNF; solid diamond), or to 6 hours of TNF followed by medium alone (TNF removal; open square). At indicated times after initial addition of TNF, mRNA transcripts encoding indicated genes were measured by RT-qPCR and normalized to *Rpl32* as described in **Methods**. However, *Rpl32* in these cells was expressed in approximately 100-fold lower amounts than in 3T3 cells. Note that only one time point was taken after removal of TNF so the kinetics of the drop in mRNA concentration are not evident. The results are shown as mean ± s.d. of triplicate samples from one representative experiment. Numbers in parentheses show the half life of the mRNA, determined by addition to ActD at 6h following TNF stimulation, which is similar to that determined at 0.5h of TNF stimulation for most genes (data not shown)

Supplementary Figure 3. Effect of TNF concentration on gene expression patterns. 3T3 fibroblasts were treated with 10 ng/ml (solid diamond) or 1 ng/ml (open square) TNF and mRNA transcripts encoding indicated genes were measured by qRT-PCR. The data are mean ± s.d. of triplicate samples and representative of three independent experiments with similar results.

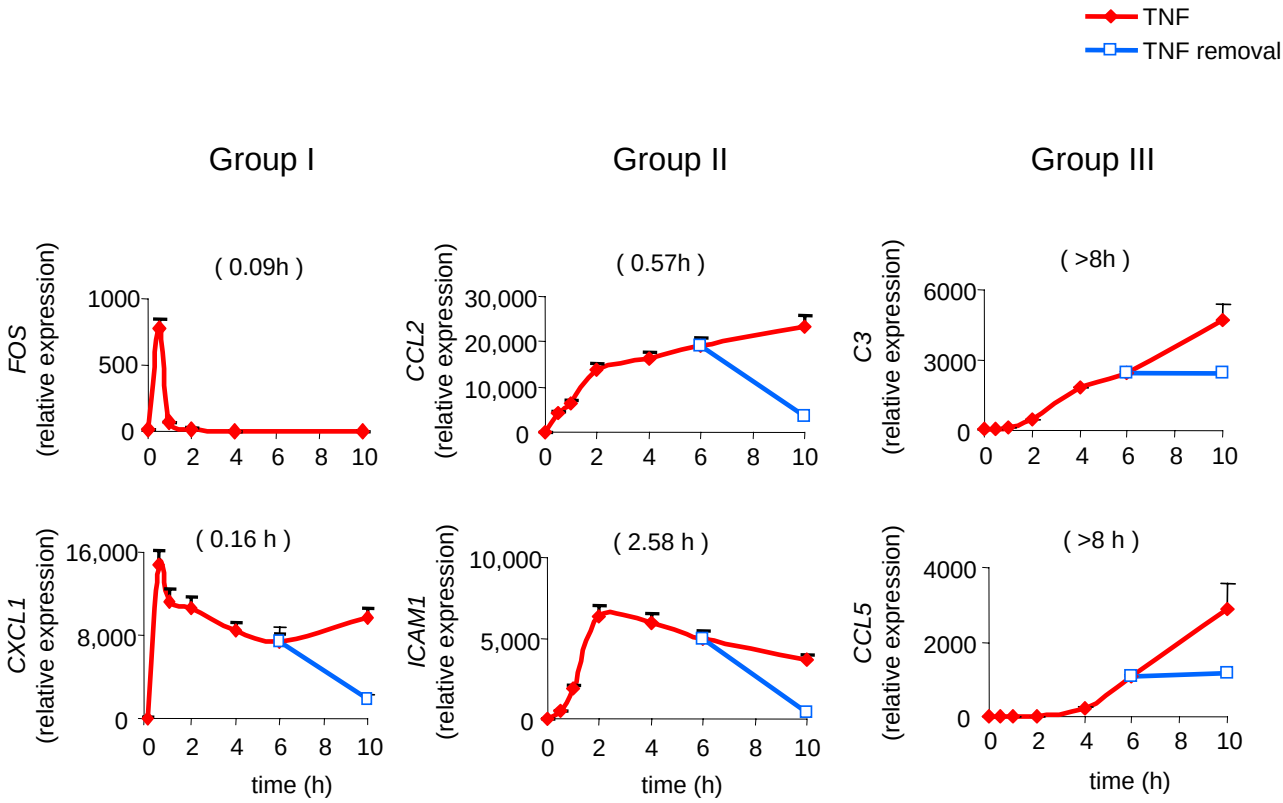
Supplementary Figure 4. Schematic of GFP transgene constructs with various promoters and 3'UTRs.

Supplementary Figure 1



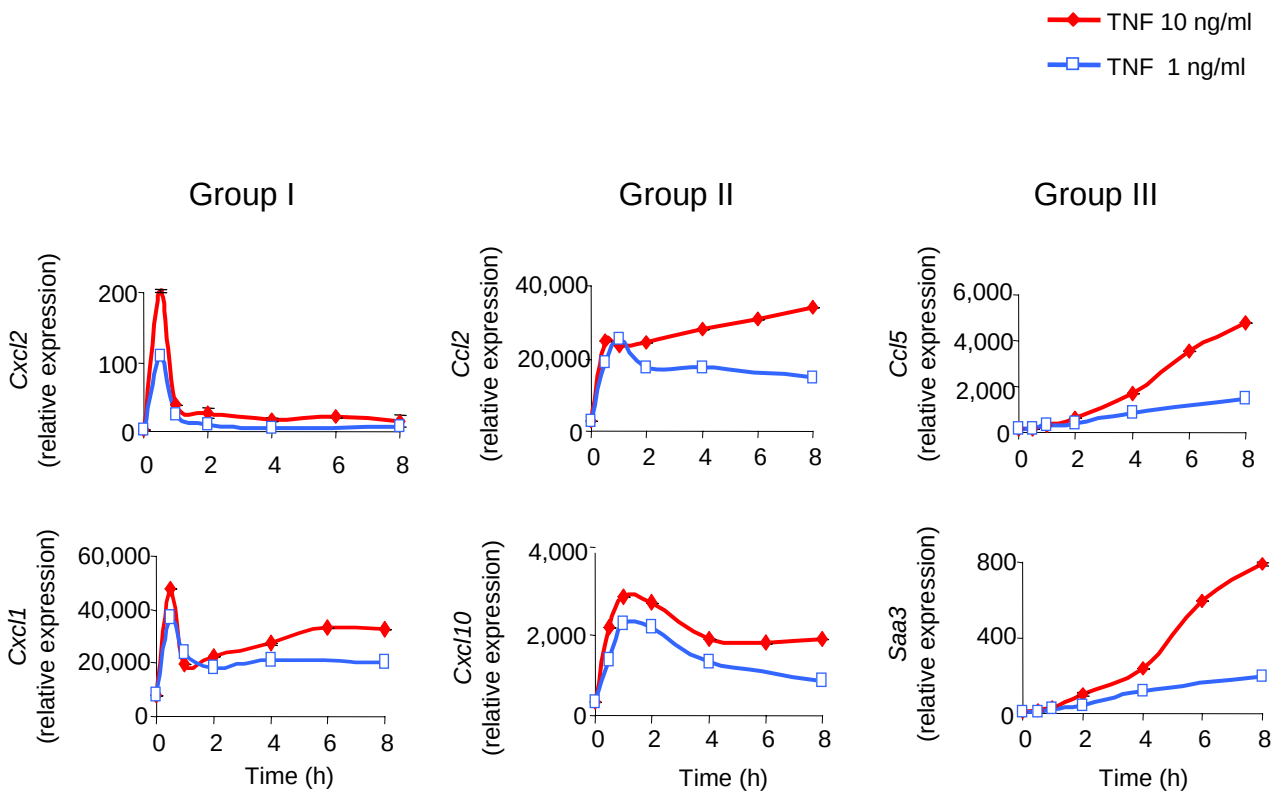
Nature Immunology: doi:10.1038/ni.1699

Supplementary Figure 2.



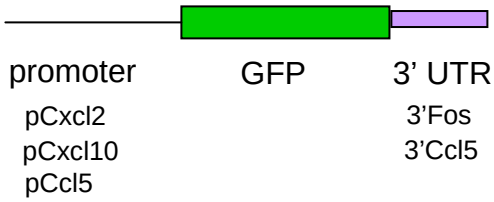
Nature Immunology: doi:10.1038/ni.1699

Supplementary Fig. 3



Nature Immunology: doi:10.1038/ni.1699

Supplementary Figure 4



Nature Immunology: doi:10.1038/ni.1699

Supplementary Table 1. List of the three groups of genes

Group I genes, (fold>=2.0, p<0.01)

Gene name	Alias, or sequence description	Accession #	relative basal level	TNF fold induction		
				0.5h	2h	12h
Blood vessel regulators						
Ptgs2	Cox-2	M94967	1.59	2.01	-1.46	-2.94
Edn1	endothelin 1	D43775	0.30	3.98	-1.19	1.02
Ereg	epiregulin	NM_007950	1.72	2.12	1.32	-1.08
Cell death, survival						
Gadd45b	growth arrest and DNA-damage-inducible 45 beta	AK010420	1.80	3.16	2.36	1.69
Ier2	immediate early response 2	NM_010499	1.20	2.35	-1.18	-1.82
Chemokine or cytokine						
Cxcl1	Gro1	NM_008176	0.70	28.08	11.98	6.20
Cxcl2	Scyb2	NM_009140	0.02	44.86	9.09	3.59
Il6	interleukin 6	NM_031168	0.31	14.20	8.40	6.30
Lif	leukemia inhibitory factor	AF065917	0.17	5.69	3.41	2.06
mRNA stability						
Btg2	B-cell translocation gene 2	NM_007570	0.24	3.07	1.22	-2.19
Zfp36	TTP	X14678	0.49	6.65	1.84	-1.04
Signal transduction						
Tnfaip3	A20	NM_009397	1.41	9.71	5.99	2.51
Ier3	immediate early response 3	NM_133662.1	5.34	4.08	2.49	1.93
Sqstm1	sequestosome 1	NM_011018	0.36	2.04	1.48	-1.00
Transcription factors or modulators						
Atf3	activating transcription factor 3	NM_007498	0.38	2.04	1.62	1.95
Axud1	Axud1	BG070296	0.31	2.45	-1.66	-4.62
c-Jun	Jun oncogene	NM_010591	2.69	2.00	1.01	-1.10
c-Fos	FBJ osteosarcoma oncogene	AV026617	0.49	4.71	-1.92	-6.42
Ifrd1	interferon-related developmental regulator 1	BB531645	0.15	3.51	1.60	-1.14
Nfkbia	IkBa	NM_010907	1.42	10.03	7.47	3.63
Nfkbiz	IkBzeta	NM_030612	0.62	5.71	3.63	2.00
Irf1	interferon regulatory factor 1	NM_008390	0.77	7.69	5.41	2.86
Junb	Jun-B oncogene	NM_008416	1.44	2.14	1.12	-1.83
Tieg	TGFB inducible early growth response	NM_013692	1.91	2.26	1.18	-1.86
Others						
Slc25a25	solute carrier family 25	BC019978.1	0.28	2.35	1.15	-1.29

Supplementary Table 1. Continued

Group II genes

(only those fold>=3, p<0.01 are shown)

Gene Name	Sequence Description	Accession #	Relative basal level	TNF fold induction		
				0.5h	2h	12h
Anti-viral and immune response						
Ifi47	interferon gamma inducible protein, 47 kDa	NM_008330	0.02	3.50	37.17	20.91
Tgtp	T-cell specific GTPase	NM_011579	0.03	1.36	24.75	9.73
Blood vessel regulators						
Gch	GTP cyclohydrolase 1	NM_008102	0.16	1.24	6.11	5.67
Cell adhesion and migration						
Icam1	intercellular adhesion molecule 1	BC008626	0.03	3.09	30.01	22.70
Vcam1	vascular cell adhesion molecule 1	BB250384	1.29	2.34	5.30	4.36
Cell death and survival						
Birc2	baculoviral IAP repeat-containing 2	NM_007464	0.35	1.53	5.25	6.27
Tnfrsf6	Fas	NM_007987	0.50	1.11	3.54	2.66
Chemokines or cytokines						
Ccl2	MCP-1, Scya2	AF065933	0.74	9.10	17.44	19.62
Ccl20	MIP-3a, Scya20	AF099052	0.02	100	100	100
Ccl7	MCP-3, Scya7	AF128193	0.34	5.90	10.53	14.09
Cx3cl1	Scyd1, Fractalkine	AF010586	0.88	1.90	4.82	2.62
Cxcl10	IP-10, Scyb10	NM_021274	0.26	10.91	31.91	17.03
Cxcl5	ENA-78, Scyb5	NM_009141	2.87	2.93	3.36	2.72
CSF1	colony stimulating factor 1 (macrophage)	NM_007778	2.53	1.90	3.00	2.10
Ch25h	cholesterol 25-hydroxylase	NM_009890	0.09	7.87	15.15	13.50
Signal transduction						
Ifngr2	Interferon gamma receptor 2	BF537076	0.25	1.26	3.01	3.04
p21	cyclin-dependent kinase inhibitor 1A (P21)	NM_007669	0.21	2.46	4.26	1.19
Ripk2	RIP2,	NM_138952.1	0.44	1.62	8.22	2.41
S1pr3	sphingosine-1-phosphate receptor 3	AV238324	0.54	1.37	3.36	3.11
Tlr2	toll-like receptor 2	NM_011905	0.66	2.67	7.30	4.79
Cebpd	CEBP beta	BB831146	1.78	1.22	4.36	1.93
Nfkbie	IkBe	BB820441	0.15	3.03	28.35	20.00
Relb		NM_009046	0.09	2.78	9.40	8.05
Tnfaip2	B94	BB233088	0.72	1.53	3.83	1.95
Npal1	RIKEN cDNA 3830408G10 gene	AK014427	0.23	1.42	3.14	1.24
Rnd1		BE852181	0.99	2.67	3.16	3.25
Tmem140	transmembrane protein 140	BC020080.1	0.44	1.04	3.32	2.36
Stx11	RIKEN cDNA 5830405C08 gene	AK017897	0.52	1.82	4.71	2.23

Supplementary Table 1. Continued

Group III genes
(only those fold >=3, p<0.01 are shown)

Gene Name	Alias, or Sequence description	Accession #	relative basal level	TNF fold induction		
				0.5h	2h	12h
Antigen presentation						
H2-D1	histocompatibility 2, D region locus 1	M86502	1.29	1.20	1.75	4.02
H2-K	histocompatibility 2, K region	BC011306	0.37	1.02	2.56	29.68
H2-L	histocompatibility 2, L region	M34962	0.23	1.30	1.70	3.66
Ii	Ia-associated invariant chain	BC003476	0.16	1.05	2.49	7.31
Psmb10	proteasome subunit, beta type 10	NM_013640	0.81	1.13	2.52	5.02
Tapbp	TAP binding protein	AF043943	4.55	1.08	1.74	3.11
Anti-viral and immune response						
C3	complement component 3	K02782	0.07	2.65	6.14	55.51
Gbp2	guanylate nucleotide binding protein 2	NM_010260	0.06	1.26	7.69	36.09
Ifit1	interferon-induced protein with tetratricopeptide repeats 1	NM_008331	0.10	-1.00	2.40	5.84
Cell adhesion and migration						
Casp4	caspase 11	NM_007609	0.04	1.86	7.81	18.72
Cdsn	corneodesmosin	BM231053	0.61	1.08	1.65	5.89
Cell death and survival						
Mt2	metallothionein 2	AA796766	1.35	1.58	3.14	5.24
Sod3	superoxide dismutase 3, extracellular	NM_011435	0.27	1.13	1.67	3.04
Serpina3g	serine protease inhibitor 2-1,	BC002065	0.06	1.11	5.65	19.18
Ubd	ubiquitin D	NM_023137	0.09	-1.08	1.71	9.14
Chemokines and cytokines						
Ccl5	RANTES, Scya5	NM_013653	0.02	-1.74	33.6	100
Ccl9	small inducible cytokine A9	AF128196	0.24	1.41	2.47	4.11
Lcn2	lipocalin 2	X14607	0.16	-1.42	1.01	4.81
Signaling transduction						
Il13ra1	IL13 receptor a1	BI081033	0.19	1.02	2.17	3.44
Il1rl1	interleukin 1 receptor-like 1	NM_010743	0.88	1.25	2.35	6.13
Naf1	Nef-associated factor 1, Abin-1	AJ242777	1.00	1.01	2.41	4.30
Tissue remodeling and wound healing						
Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	BC003264	0.30	1.08	1.74	13.07
Mmp13	matrix metalloproteinase 13	NM_008607	0.15	1.53	4.86	16.48
Mmp3	matrix metalloproteinase 3	NM_010809	1.37	1.20	1.86	6.57
Serpinf1	, PEDF	NM_011340	2.18	1.09	1.26	4.08
Ppicap	peptidylprolyl isomerase C-associated protein	NM_011150	0.20	1.17	1.20	3.07
Others (unknown function)						
1110004C05Rik	RIKEN cDNA 1110004C05 gene	BC010291	3.38	1.24	1.97	3.77
Abca1	ATP-binding cassette, sub-family A1	BB144704	0.07	2.07	2.30	7.08
AI561871	expressed sequence AI561871	BI143915	0.17	-1.20	1.51	5.08
AI882074	expressed sequence AI882074	BB730912	0.09	1.29	3.32	5.91
Arts1	ESTs	AV287655	0.10	1.16	1.83	3.59
Lhfpl2	lipoma HMGIC fusion partner-like 2	BG917242	0.02	1.82	6.77	23.29

LOC677168	cDNA, RIKEN clone:2900034J12,	AK019325	0.25	-1.06	2.32	5.91
AW049765		BC026642.1	0.10	-1.41	2.57	21.95
Prnd	prion protein dublet	AF165166	0.02	1.18	3.38	28.41
U90926	cDNA sequence U90926	NM_020562	0.38	-1.16	1.03	3.72

Supplementary Table 2. Stability of mRNA transcripts measured using two different approaches

mRNA stability (half life, h, mean ± s.d., n=3)

	Genes	6h TNF pretreatment	
		TNFa removal	ActD treatment
Group II	*Ccl20*	1.30 ± 0.12	3.33 ± 1.02
	Ccl2	1.38 ± 0.09	0.82 ± 0.01
	Ccl7	1.56 ± 0.21	1.32 ± 0.06
	Tlr2	1.93 ± 0.25	1.27 ± 0.32
	Nfkbie	1.69 ± 0.07	1.90 ± 0.13
	Cxcl10	1.87 ± 0.05	1.92 ± 0.05
	Icam1	1.66 ± 0.20	2.30 ± 0.56
	CSF1	5.33 ± 2.51	2.60 ± 0.43
	Mmp10	10.5 ± 18.0	stable
Group III	*Ifit1*	stable	1.97 ± 1.22
	Stat1	9.76 ± 18.5	11.7 ± 12.7
	C3	stable	stable
	Ccl5	stable	stable
	Mmp13	stable	stable
	Mmp3	stable	stable
	Saa3	stable	stable

Supplementary Table 3. Sequneces of qPCR primers

name	alias	species	primer name	sequence
Tnfaip3	A20	mouse	A20_(1)_F	GAACAGCGATCAGGCCAGG
			A20_(1)_R	GGACAGTTGGGTGTCTCACATT
actb	β-actin	mouse	actin_F	AGGTGTGCACCTTTTATTGGTCTCAA
			actin_R	TGTATGAAGGTTTGGTCTCCCT
C3	Complement 3	mouse	C3_(2)_F	CTGAGAAGCGTCTCCATCAAG
			C3_(2)_R	ACGGGCAGTAGGTTGTTGTC
Ccl2	MCP-1	mouse	Ccl2_F	CTGAAGACCTTAGGGCAGAT
			Ccl2_R	AAGGAATGGGTCCAGACATAC
Ccl20	MIP-3α	mouse	CCL20_F	GCCTCTCGTACATACAGACGC
			CCL20_R	CCAGTTCTGCTTTGGATCAGC
Ccl5	Rantes	mouse	Ccl5_(1)_F	GCTGCTTTGCCTACCTCTCC
			Ccl5_(1)_F	TCGAGTGACAAACACGACTGC
Ccl7	MCP-3	mouse	CCL7_(1)_F	GCTGCTTTCAGCATCCAAGTG
			CCL7_(1)_R	CCAGGGACACCGACTACTG
Ptgs2	COX-2	mouse	COX-2_F	TGAGCAACTATTCCAAACCAGC
			COX-2_R	GCACGTAGTCTTCGATCACTATC
CSF1	M-CSF	mouse	CSF1_(2)_F	AGTCAACAGAGCAACCAAACC
			CSF1_(2)_R	CAAAAATCCCTCACTAGCCTCTC
Cxcl1	KC	mouse	Cxcl1_(1)_F	CTGGGATTCACCTCAAGAACATC
			Cxcl1_(1)_R	CAGGGTCAAGGCAAGCCTC
Cxcl10	IP-10	mouse	Cxcl10_F	AGGACGGTCCGCTGCAA
			Cxcl10_R	CATTCTCACTGGCCCGTCAT
Cxcl2	MIP-2	mouse	Cxcl2_(1)_F	CCCTCAACGGAAGAACCAAAG
			Cxcl2_(1)_R	TTCCCGGGTGCTGTTTGT
Edn1	endothelin-1	mouse	ET-1_(1)_F	GCACCGGAGCTGAGAATGG
			ET-1_(1)_R	GTGGCAGAAGTAGACACACTC
Fos	c-Fos	mouse	Fos_(2)_F	CCCATCCTTACGGACTCCC
			Fos_(2)_R	GAGATAGCTGCTCTACTTTGCC
Icam1	ICAM1	mouse	ICAM1_F	TGTCAGCCACTGCCTTGGTA
			ICAM1_R	CAGGATCTGGTCCGCTAGCT
Ifit1	Ifit1	mouse	Ifit1_(1)_F	CTGAGATGTCACTTCACATGGAA
			Ifit1_(1)_R	GTGCATCCCCAATGGGTTCT
Nfkbia	IkBα	mouse	IkBa_F	CTGCAGGCCACCAACTACAA
			IkBa_R	CAGCACCCAAAGTCACCAAGT
Nfkbie	IkBε	mouse	IkBe_(1)_F	TGGACCTCCAACTGAAGAACT
			IkBe_(1)_R	TTCCTCTGCAATGTGGCAATG
Il1b	interleukin-1β	mouse	IL-1b_(1)_F	GCAACTGTTCCTGAACTCAACT
			IL-1b_(1)_R	ATCTTTTGGGGTCCGTCAACT
IL6	interleukin 6	mouse	IL6_F	TAGTCCTTCCTACCCCAATTTCC
			IL6_R	TTGGTCCTTAGCCACTCCTTC
Irf1	Irf1	mouse	IRF1_(2)_F	AGGCCGATACAAAGCAGGAGA
			IRF1_(2)_R	GCTGCCCTTGTTCCTACTCTG
Jun	c-Jun	mouse	Jun_(2)_F	ACTCGGACCTTCTCACGTC
			Jun_(2)_R	CGGTGTAGTGGTGATGTGCC
Rpl32	L32	mouse	L32_F	AAGCGAAACTGGCGGAAAC
			L32_R	TAACCGATGTTGGGCATCAG
Mmp10	MMP-10	mouse	MMP-10_(2)_F	AACACGGAGACTTTTACCCTTTT
			MMP-10_(2)_R	GGTGCAAGTGTCCATTTCTCAT
Mmp13	MMP-13	mouse	MMP-13_(2)_F	ACCTCCACAGTTGACAGGCT
			MMP-13_(2)_R	AGGCACTCCACATCTTGGTTT

Supplementary Table 3. Continued

name	alias	species	primer name	sequence
Mmp3	MMP-3	mouse	MMP-3_(2)_F	TGTCCCGTTTCCATCTCTCTC
			MMP-3_(2)_R	TGGTGATGTCTCAGGTTCCAG
Saa3	Saa3	mouse	Saa3_(1)_F	TGCCATCATTCTTTGCATCTTGA
			Saa3_(1)_R	CCGTGAACTTCTGAACAGCCT
Serpina3g	Spi2A	mouse	Spi2A_(1)_F	CTTCCCAACGGCTGGAATCTA
			Spi2A_(1)_R	ACTGTCCAATCAGGCATAGCG
TLR2	TLR2	mouse	TLR2_(3)_F	CCAGACACTGGGGGTAACATC
			TLR2_(3)_R	CGGATCGACTTTAGACTTTGGG
Tnf	TNFα	mouse	TNF_F	CTACTCCCAGGTTCTCTTCAA
			TNF_R	GCAGAGAGGAGGTTGACTTTC
Vcam1	Vcam1	mouse	Vcam1_(1)_F	AGTTGGGGATTCGGTTGTTCT
			Vcam1_(1)_R	CCCCTCATTCCTTACCACCC
Zfp36	TTP	mouse	Zfp36_(1)_F	TCTCTGCCATCTACGAGAGCC
			Zfp36_(1)_R	CCAGTCAGGCGAGAGGTGA
Zfp36	TTP	mouse	Zfp36_(2)_F	TCGAAGAGACCCTAACCAGGC
			Zfp36_(2)_R	GCGTAGTCATCAGGATCGGA
C3	C3	human	hC3_(1)_F	CCTGCTACTAACCCACCTCC
			hC3_(1)_R	AACAGTGACTGGAACATCCCC
CCL2	MCP-1	human	hCCL2_(1)_F	CAGCCAGATGCAATCAATGCC
			hCCL2_(1)_R	TGGAATCCTGAACCCACTTCT
CCL5	Rantes	human	hCCL5_ F	CCCAGCAGTCGTCTTTGTCA
			hCCL5_ R	TCCCGAACCCATTTCTTCTCT
CXCL1	CXCL1	human	hCXCL1_ F	CTGCGCTGCCAGTGCTTGCA
			hCXCL1_ R	TGTGGCTATGACTTCGGTTTG
CXCL10	IP-10	human	hCXCL10_(1)_F	GTGGCATTCAAGGAGTACCTC
			hCXCL10_(1)_R	GCCTTCGATTCTGGATTCAGACA
FOS	c-FOS	human	hFOS_(3)_F	GGGCAAGGTGGAACAGTTATC
			hFOS_(3)_R	CCGCTTGGAGTGTATCAGTCA
GAPDH	GAPDH	human	hGAPDH_F	AACAGCGACACCCACTCCTC
			hGAPDH_R	CATACCAGGAAATGAGCTTGACAA
ICAM1	ICAM1	human	hICAM1_(1)_F	TCTGTGTCCCCCTCAAAAGTC
			hICAM1_(1)_R	GGGGTCTCTATGCCCAACAA
NFKBIA	IkBα	human	hIkBa_(1)_F	CTCCGAGACTTTCGAGGAAATAC
			hIkBa_(1)_R	GCCATTGTAGTTGGTAGCCTTCA
IL6	Interleukin6	human	hIL-6_(1)_F	AAATTCGGTACATCCTCGACGG
			hIL-6_(1)_R	GGAAGGTTCAGGTTGTTTTCTGC
Rpl32	Rpl32	human	hL32_F	AGCTCCCAAAAATAGACGCAC
			hL32_R	TTCATAGCAGTAGGCACAAAGG
GFP	GFP		GFP_(BMC)_F	GGAGCGCACGATCTTCTTCA
			GFP_(BMC)_R	AGGGTGTCGCCCTCGAA
GFP	GFP		GFP_(6)_F	ACTTCAAGATCCGCCACAACA
			GFP_(6)_R	TGGGTGCTCAGGTAGTGGTTG